

University of Dundee

DOCTOR OF PHILOSOPHY

Identification of MMS22 as a regulator of DNA repair

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# Identification of MMS22 as a regulator of DNA repair

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2010

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Q96HA7\_HUMAN 1 MSL.....ERELRLQSLKAKAKAQRAGORREAAALCHOLGELLAGHGRVAEALAEQHWQELQIRERADDPGLCAVAHRKIGERLAEMEDYPALLOHCHOYLELAHSLRNHTLQRAWATIGRTHEDIYDHC.....QSRDALQAAAEKSLIAVDEELGTLAG.....  
A9J7R8\_DANRE 1 MTS.....TKKIKQLOKAKSKAQSNNLKEEASLNCOLGEYVAKTDQYQAAEEHROBLAISEILHIVDGSAYANKRIGECYAEELGNIEBAALKHORHLNARSVHDAEQRALATIIGRTYLFIFDSD.....QSANSLKHAEDAFKRSIAVDEELGTVSP.....  
B0VZJ6\_CULQU 1 MSSE.....TDVEQRLLRRKKKAASEGNLLLEAEARLKEGEMYHEGSEHRKALIEYKLVAKAFONLKMQMELGRAHMMIGEQNNMLGEPEKALQYDRSYDIAKQOKHIVQVQRAHVITIGRTIFLMKGQSCBKIL..EQAMEPIHEAEKFSRSLKSRLEIK..SIGR.....  
Q8MT49\_DROME 1 ME.....EKRYLKRKEKASRDNQDQAVASVNCOLGDFYNOCKYTDVAVREYVQBAQIYASMGKELETAKKKRMYGEMVLTLCDDYAAKHDINDYLIKTAKRLLKNQVREQRAYATILGRVHLLHGQSLADSSAGSCMBOKLAEKFNLRSLLLIKLSDQISQK.....  
B9F3L2\_ORYSJ 1 MGRGGGGRWTKEEEEELKAAKRGYREAVAGNREBEARAVNIGDILHRRGEVVEALRWLIDYKVSXYLPRQRLHLLPSCQSLGELVHRLGNSEALTYQKHLQALAEANDTVEKQRACTQLGRTYHEMFLKSD.....DCEATQSAKKYFKKAMPALQILKEKPPPGSSSGFLLEY  
Q6Q4D0\_ARATH 1 MGRLL.....VVAAKKRAYKNAEEVGDREARWANNVGDILKNHGEYVDALKWFRIDYDYSVKYLPKGDLPTQCSLEIILRLNEFEPAIYQKHLQALAEANDTVEKQRACTQLGRTYHEMFLKSD.....DCEATQSAKKYFKKAMPALQILKEKPPPGSSSGFLLEY

Q96HA7\_HUMAN 155 .....GLENMRTLYLNLGLTFESLQQTALCNDYFRKSTFLAEQNHLYDLFRARYNLGITHW..RAGOHSQAMRLEGRECHAHMRRKRFME..SCCVVIAQVLDLSDFLAAKRAKKAYLGSQKVPORAAICQNLQHVLAHVRL  
A9J7R8\_DANRE 155 .....REISEMKARILLNLGCVYDGMKEPQRCSDLTFRQSTIYAEKNLLLEDLYRANFNLSGITHF..RNGOHSRAMRCFEQSKCEKARKMKDKFSE..SECFHSIGKILLHLGDFSAARRSLKAKAFCLGSQQPSDREAVKMKFRHAIKGCQL  
B0VZJ6\_CULQU 159 .....LEQVMEARSLNLNGVTKHEQGNNEQATEYMOKATKLAENNDLTLLHQCYTTSALLFNSKLNHARALKALSEALEVASRLQNKATKMCETLITKADILINTGDFQSAHQALQKQAYLRTIPVADTADNTERRLKVLVAVGRV  
Q8MT49\_DROME 156 .....LEQLDMQARCYLNGVKEHMEAPQESIBYIDKATKISKTHELMDLTHLCYISMSLLYICKNDATAALRFCNMALVAKRFPNKVKKICETLITKAEILIKAGDFASAKQILIKAYAKNTPENDRNVIEKQRLIVVKVQCT  
B9F3L2\_ORYSJ 174 IDAYNNMGMLELDLDNYEEAEKLLVQGLKIDEEEVHOYDARSRLHNLGNVYIELRNWNRAKHIEKDTEICRKIRHTQGEAKGFINLGEVHS..RVQKVEDAKLYCNKALQITKCLEDEBDALMDO..IHQNIETVTKAAKVLMEKMTDEQKLAKLRVDRDTSNARGTSKERKLLLEQYAW  
Q6Q4D0\_ARATH 164 INAHNNMGMLDLDLDNPEAARTILKGLQIQDEEEVRYDARSRLHNLGNVYIELRNWNRAKHIEKDTEICRKIRHTQGEAKGFINLGEVHS..RVQKVEDAKLYCNKALQITKCLEDEBDALMDO..IEHNTKIVKRSKVMVEELREELMLKLKLSAEMTDAGKTSBERKSMLOQWAC

Q96HA7\_HUMAN 296 QOOLEEAEGRDPOGAMVTCOLGDLFSKAGDFPRAABAYQKOLFRALLDRPGAERAIHVSIATLTGMDKHGHAVRHYEELRLERS..GNVLEAKTLNIALSRLEAGDAYELLAPCEKALKS.....CAQQAQRPO..LORQVQHLHTVQ..LRQPQEA..PETETRLRELSVA  
A9J7R8\_DANRE 296 EQTAAEVTQKFSHEALDLSBOLGDLYCKVGCYKALEAYQTQLACAEALAKPALEIAVHVSIATTYDLRQHHRAVEHYRQELQLRK..GNPKECECTWLNMAVCQCEMCQSMETLDHCFSTALN.....CAEKSGLNK..LORRVLRVWLQAO..RRCGSSQC..DDEARLMEICER  
B0VZJ6\_CULQU 302 EDEIMTGSEERYKKGLYERMGDGACKLENYAKAIDYYLKMLEACQALAGEADRDLIPIYVSYLYQTYKONKQYDDALVYLWQYELID..DPPEAYNTLLSIADVFQAQKKSWNVEDEIYQARA.....QAKKLKSLP..KERVATKRCVAML..KRCGEMMAERLEKEATCGMMD  
Q8MT49\_DROME 309 LDEIVLTSSVDYAKKGLYERKLDGCGCHLMNVEKALTYQKMLENAELNVEKSGSKVPIIYVSYLYQTYKONKQYDDALVYLWQYELID..DPPEAYNTLLSIADVFQAQKKSWNVEDEIYQARA.....QAKKLKSLP..KERVATKRCVAML..KRCGEMMAERLEKEATCGMMD  
B9F3L2\_ORYSJ 351 LDNLIM.....EKARMITAWPKLEKFSQKQKRVANLH..DKKQNSLVAIYGEYSQKLRNFKSKARKKWCNMWYRSIENLEGGALAKVNIENVLDSQCDWAG..ALQAYEEAYRQCYLAMLISVGEGLSNVLDALENHYSYHMYVRFDNIEEAKKQOEDSKRM  
Q6Q4D0\_ARATH 341 LGSLLI.....DKSMVFAVLEKHLQYKRRKKISLECL..DKKELDAFMIVGESYQNLNRNFKSKIKWIFRISYENIENLEGGALAKVNIENVLDSQCDWAG..ALQAYEEAYRQCYLAMLISVGEGLSNVLDALENHYSYHMYVRFDNIEEAKKQOEDSKRM

Q96HA7\_HUMAN 463 EDEDE..EEEAETAAATA..ESEALEAGEVE..LSEGEDDDT.....GLTPQLEDE..ELQ..GH..L.....GRRKGKRWKRRNDMGETLHFRACIEGOLRRVQDLVROGHPNLNPROYCGWTLPHBACNYGHLEIVRFLDHGA..AVDDPBGQGGEGITPLHDLALNCHEFVEALLIE  
A9J7R8\_DANRE 463 DGLSL..DQSEDDEDEVDNNEPLEDSDIQ..YSES..DDED.....LEGDY..K..MV..T.....GRRKTQRWNRNRNKEGETLHFRACIEGOLRRVQDLVROGHPNLNPROYCGWTLPHBACNYGHLEIVRFLDHGA..AVDDPBGQGGEGITPLHDLALNCHEFVEALLIE  
B0VZJ6\_CULQU 470 LENSVAEDSDSDSDTQDETETISIEYAINSLGEIDVDLAELSNSDD..ER.....PKPLDLSLE..GKNT.....RKRGTTFKYKNNKNGESQLHACIEGOLRRVQDLVROGHPNLNPROYCGWTLPHBACNYGHLEIVRFLDHGA..AVDDPBGQGGEGITPLHDLALNCHEFVEALLIE  
Q8MT49\_DROME 470 LDOEBE.....SVGCDEEESGGGTAVQONTPDWDDFDLATALDTSDA..SD.....LDTEKPRP..QRT.....TGNRLTLV..KNNKGETQLHACIESNIEVRRRLDQGHTVNVRDHAGWLPHEACNHCYREIVELLLKGAASAINDKGTSDDGITPLFACSNFGLDAELLID  
B9F3L2\_ORYSJ 510 SDQHEARDTVSYCYSTESE..DGNVSDNLTINTEINDGNIANN.....ISEEFDVVLASLVHKSXSSTKASKIHSSP.....  
Q6Q4D0\_ARATH 492 EHAEKACSTQDECSSTDSGHANVSNDPRNACSSPQTNSLRSEKRLADLEANDVPLISFLQPKGRFLPKK..QV..SGKQ.....

Q96HA7\_HUMAN 620 RGASVTLRTRKGLSPLETLOQWVKLYRRDLDTQKAR..AMEMLLQAAAS..GQDPH.....S..SQAFTHPSSLLFDPETSPPL..SPCEPPSN..S..TRLPEASQAHVRVS..PGQAAPAMARPRSRHGPAS.....SSSSSEGEDS...AGPARPQKRPSCSAT..AQWA.....S  
A9J7R8\_DANRE 614 RGASVTVRNSRGHPIDTLQWFKTYISGGLDPETKQECL..ETEKILKRLAS..GDVSVVCAAPRQKQELQDSOLFDEAYSEPLLRSPSPPPITRPAATVPTSKD.....SA..PKHRS..TASSTRPGRMEVDVLYGDDSSSDNPDSDCLSPLEVRPSRSPFPAGSQBPVPSQELP  
B0VZJ6\_CULQU 635 KGANCTORTDSDDITLNLVQLWFGVQKKLAPETIISYNTIYHRIKGYFVDAVAKRPD..E.....SATVPDALINDS.....QPA.....GRSTR..RAAQPI..RSGSESGNEETRSARS.....TVRNSRSPKSRRLP..PEVRSSGSL  
Q8MT49\_DROME 632 RGADATVTDYNEICIAQIDKNRQGAQ..LVDGQAQYQAQ..LREKILRLTSLKVGICSD.....K..K..NA.....REL.....TFNFA..KRISREERGSMSEEDDEEALHES.....NKRSL.....SHNRSQ..SEY.....G..  
B9F3L2\_ORYSJ 584 NVDESODMDSPEEV..VSKS..FSNH..SGRRK..VRV..VISDDEABEAPEDQ.....SKRTLTGRA.....  
Q6Q4D0\_ARATH 571 .....DADT.....DQTKKDFSVVADS..QQTV..AGRRK..IRV..LISDDESETEYELGC.....PKDSHKLVRQNE.....

Q96HA7\_HUMAN 772 WTPGPASNR..EAATASTRAAVQAIRGVGSAQSLRG...GPRR..GHSKA..LAPQAALPIEEBCL..AGDWLELMPILT..RSRRPRP..RGTGDNRRPSTT..SG...SIA.....DSE..ESRPRARAKOVR  
A9J7R8\_DANRE 785 SVYGIKETT..VPPQSESGRLVEYQKAMNGLSASKRLFSQSLDSFAFTSPAVSANSRAALVPEDQYL..ADDWLEDDLIDMOPKRRVSEHNATRETTIRS..QNNSSSTIA..EVP.....PR.....VQ..SC..SS..RGSLSLKKGSNKPVRV  
B0VZJ6\_CULQU 761 SSDSEPEEQIRPRASKPGVDFYOTAIEAVRRK...TNA..QLSLP..KDPNP..APSKRTAHMREEV..GDDWLVADVPAT..KQKFLSDKDYSEPSVSSRRSLEDL..VS..PKQSV..SS..KGSNRARQSVSLDPAPDANQILMSANRSFSRAPASQSKSHRSQ..LTGS..NRYCS  
Q8MT49\_DROME 737 ..AKK..SK..SSTQPSASKEYRSVMAHLKRPNL..N.....DPTP..STSLT..NKKHKNFALSDEEV..DADNLLIDVGPGR..KRRKINGSD..LSR.....RTSKENFQDALTSLPANWEDDLQ.....ATPEN.....EYSORQKQMRKLTLRSSSSMSS..NHSS..ATSSRKHQAT  
B9F3L2\_ORYSJ 639 .....DSLSTSE.....RIANAANRN..RNQHTS.....HPITKEVDSVCTCPAEESICSPFKSGPVCHG.....N..N..DGP..DLG..ASST..G.....KLSV..SK.....P..AA..SG..SKGVTH.....A..S  
Q6Q4D0\_ARATH 628 .....EVSEESM.....YFDGAINYT..DN.....RAIQDVEEGSCSYTLPHPKIA.....P..NVS..NCR.....SLSN.....G.....IAVET..TG.....R..RK..KG..SQCVG.....D..S

Q96HA7\_HUMAN 881 LTCMQSCAP...VNAGPSSLAS.....EPGSPSTRVSE.....PSGD..SAAGPLGPAPPP...IRVRVQVDHFLFIPVPHSS...DTHSVANLAEQAQRY.....YQTCGLPRLPRLT..KEGALLAQLIPDVLQ...SNDEVLAEVTSNDLPLTDRYRACQSLGO  
A9J7R8\_DANRE 920 MNOLPGMV..M...LGRREYSR.....SQ..SPMITQESDHQEPAPPHQMPASSPQNRAAHVPAIRMRVYVQDNVFLIPVPHSS..ADSCVIANLQDQAQRY.....YQTCGLPRLPRLT..KEGALLAQLIPDVLQ...SNDEVLAEVTSNDLPLTDRYRACQSLGO  
B0VZJ6\_CULQU 924 LLEAGFSVSS...RSVGSNGSAVDDPEDV..RLLMSPK..ESVA..SSSG...DNRP..SGMITTKAGFLVLP..SMVRVYVQDQIDVYDQDQ..EMGLSVGNLAEVAKRY.....GKHKGRPLKLMRSDNLSMDSEPLSTYLE..KTDPIKSYVIEYTSLRGDFYDSCRLDR  
Q8MT49\_DROME 845 LLDGFSRFRSESPLGSESDGTTSLISVRTIEPDDSTTSTQY..VLISPAK..SSPIKQVATP..VLATTVSFKVYKIDELLVPIERKK..LDQINIRLNAEEAGRYH.....NKLGTPLRLKLTADGAYEYEDTPVSVALE.....QNMIMASLDWKSIP..SQRYEEMCQKOK  
B9F3L2\_ORYSJ 723 .....NSRQO...G..L.Q...SSDA..DKFWFKIGELLYLDANACTCEGAFSECLKVEAVCYVLIQIPDEKRSKGLPIITGELCKCKGVLDITSRDYDQLASEQOCQDVDDWVFKRMKLYVDFCTKSE  
Q6Q4D0\_ARATH 701 .....NGTSCKT.....G..AA.....LV.....N..F..H.....AYSKTEDRKIKTEIENEHIALDSCSHD.....DESKVLTCLYVQLPDPDEKSKGLPIITGELCKCKGVLDITSRDYDQLASEQOCQDVDDWVFKRMKLYVDFCTKSE

Q96HA7\_HUMAN 1029 GEHQOVLQAVELQGL..GLSFSACSLAI...DQQLTPLLRLKLTALRELRAGNRGLGKCVAEVVAALGTM...PSLALLDSSNHLGPEGLRQIAMLG...PGQATLQSEELDLNMPNLGCGCGQSILASLLHA...CPLSLTLRQACGFGPSFSLSHQTLGSAFQDAHEKILSLIS  
A9J7R8\_DANRE 1073 EENRVRVRVCEVQBS..SSCVSVCGLSI...SPAELNPLRLAKLTQASLTETLRIANRINDELLPEMMAAAAT...PRLRVLDLSANQITGEGRLKASDAFETRSQAAPFCLEELNLSMNPGLGCGWTQALASLLSS...CPLSLSLSLQACGLSARFLQOHRLLANAMASTGNMRSVCLIS  
B0VZJ6\_CULQU 1084 EYVITALMSANLMEN..TGKALKRDFAGTTRQDFVIFQALGCGSSTRELNLSMNPQDDELQGFVEKEPVL...KNLERENLAMPNLTKQSFMSSTKL...ASLPDMIYNTLDELDRSCLSLDQSMPLASICQR..MEQRLVRLASTMITNLTYL...GSPPLDVRVQVVDVS  
Q8MT49\_DROME 1045 TVDNKVKLLIERSQN..NMMLSEGLWM...RAEKTEPFFKALLHQARLTVLDSLGNFTGNEGCGQIAKSEPLTL...LQKALRIQCNALGSHGEALLGCG...GMDKLELEELNLNQNPLGNASVRLISKYCASPAQALITCQLAQCELETL.....QDFDLFGNKLTRFDIS  
B9F3L2\_ORYSJ 853 APNNKLKKLYNLEVSDEIVISDCGL...QDLSTIPFDALRLAKTIAVLDLSHMLMGNTIETIERQYISSSSQTYGGLTLDLHCHNRFPGTALFQICE...CAMVNRNFGNLSNAGMLPDACGSYFTILQK...CKALYSLNVEQCSITSTRVQ...KMDALHEGSAHSLISG  
Q6Q4D0\_ARATH 825 KPSMKLKKLYISEV..EDDINVSCEI...QDIAAPALLCALHVI..NLAMLDLSHMLMGNTMEKIKQLFASSSQMGYALTLDLHCHNRFPGTALFQICE...CPVLFTRELVNVSRRNRTDAGSYLSTVKN...CRALYSLNVEHCSLSTRITQ...KVANALDSKSGSLQICG

Q96HA7\_HUMAN 1198 YNA..GAPALARTIQSP..AGTLHLLELSSVAAGKGS...DLMPEVFRYLAKECG.....ALAHITLSANHLGKAVRDLRCRIS..LCPSEILSLSANPEISCASLEELLSTQKRP..QGLSFTIGSGCAVQGPLG...LGLWOKT.....  
A9J7R8\_DANRE 1244 HNA..LGSTGFELVKTDP..MHCITHELSAVCRGPSQ...PSMELITKLQAGDC.....PLTHNLSCNGLTBDHSLVLLARCIP..VCPSEVSLDLSANPLVTSTGLHSLINGLVEAR..RPLGHNLNQCQVSGPLA...EDCLDSL.....  
B0VZJ6\_CULQU 1248 ENS..LNKKSIEYMFAPKD..MCILTELNVCKLGLLAEF...K..PNLTVATQKFEF.....DMLSTNLNLCGLTDESLTLVPIRSSAGKRLDVSFNRLQKSFVEVFTINTHSL...EMVREAE..NPL..VLKGLSDNMLMDQ.....  
Q8MT49\_DROME 1206 FNO..ITQGSVRRITDLDN..SCRLEQLNLGYVRWPLDDASGAFALSERVLTFEGGTG.....ERFVQIACCGNLDNAHMVNIQSHIA..KAKOELGSLDLSNLSGTTLYLDELPLQLR.....VNTC..NLDDRLDR.....  
B9F3L2\_ORYSJ 1019 NNPNISGNTMLSLSLKSLASLKRFSLSITGRKLSKLM...VDK..LCVLQAQSS..CLSGFLPGTYIGSGGATKLTALSCASQELRLDLNLCGLTIPDFDSCNTNIS...QINTVDNLNGGS..FULEECDAITRALLSNPQ..CSIRSITIDRCNLGLAGT...VGILOALAGNDQL  
Q6Q4D0\_ARATH 989 XNPNVSGSSIQNLAKLATLSFSFAELSMNGCKLSSQV...VDS..LYALVKTP..SLSKLLVGSSGIGTDGAIKVTESLCYQKEETVKLDSLCCGASSFFIKQNDYPT..LTSSLELNVGNGNP..ITEEGISALGELLRNPC..SNIKVILSKKGLKLAGL...LCITQALSDNNKL

Q96HA7\_HUMAN 1331 .....AAQLREILQCSRRIC...AEDRALQLOPSRPGP..GECTLDH.....GSKLFFRRL 1378  
A9J7R8\_DANRE 1377 .....SDHRLDRCSQSLN...KLDQDALQOSKRRRT..E..AVHIFSR.....NSKMKLSTSSPSH 1427  
B0VZJ6\_CULQU 1380 .....YDRARCPYAVDLMRPLRIGEPE...AKTLIKLITDFEQLWKERGAVMSKST.....VSLRKHYT 1439  
Q8MT49\_DROME 1383 .....LQK...EQLOKPLRELTIEVDQVSMGPALDLSQIQLOLQFGDKAKMLTTSNSRKIGR.....RYKGLKLLADGSAE 1405  
B9F3L2\_ORYSJ 1132 EELRVAENTNLALQRTLOYDEAQDVSPGTQDQNRNANANDHIDDPDKMEVPDSEDEAAVHEDTRAATGPDGSCASSQCRNSSSGCHATAIGLADAIISAKQLVLDISNGLS...EEDIQSYLWASGPRGDKARKHVAKEVHVFAVGMNCGKLPCCRRLDQ... 1346  
Q6Q4D0\_ARATH 1153 EELNLSDNAKIEDETVFGQPVKER...SVWVEQHGCTKSVTSMDEQELCETNMCEDDLEVADESEDEIEGATSSSLSPRKNHIVKELSTALSMANQIKILDISNNGFS...VEALETYMSSSSSSSRGTQARHVKETVHFYVEGKMCQGVKSCCRKD... 1311

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